

*✓2* OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/875,321

DATE: 06/21/2001  
TIME: 17:19:21

Input Set : A:\10448-061001.TXT  
Output Set: N:\CRF3\06212001\I875321.raw

ENTERED

4 <110> APPLICANT: Curtis, Rory A.J.  
6 <120> TITLE OF INVENTION: 52906, 33408, AND 12189, NOVEL POTASSIUM  
7 CHANNEL FAMILY MEMBERS AND USES THEREOF  
10 <130> FILE REFERENCE: 10448-061001  
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/875,321  
C--> 12 <141> CURRENT FILING DATE: 2001-06-06  
12 <150> PRIOR APPLICATION NUMBER: US 60/209,845  
13 <151> PRIOR FILING DATE: 2000-06-06  
15 <160> NUMBER OF SEQ ID NOS: 13  
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
19 <210> SEQ ID NO: 1  
20 <211> LENGTH: 3525  
21 <212> TYPE: DNA  
22 <213> ORGANISM: Homo sapiens  
24 <220> FEATURE:  
25 <221> NAME/KEY: CDS  
26 <222> LOCATION: (638)...(3178)  
28 <400> SEQUENCE: 1  
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30 tcccgcagcg gccaaggcag ggctcaggcc ccgggattct ccccacacgc tgctgcactg 120  
31 ggcgcggcgg tcgccaaact ttttctcccc aaagccagtg ccccccgcagt tacttggcgg 180  
32 gcaagccggca gcccactctc ggcgggatga tctggagaa gcgggcgtgg gacgaggggg 240  
33 ctgctgtttt gcagccctgc gaggcgtgca gtcggagaag tggctgggggt tccacaccgt 300  
34 ccctgagcct gccccctggc caaggtggcc cgacgtgctg cagtggctgg cgcagggtat 360  
35 ccgggcagcg cgtccggcac tagtcaaggg ggcagcggca cggggaggag gggcccttt 420  
36 ctcttttctc ctccccctgc agcccaagctg cactgcgtgg gggctctcca tctccacgc 480  
37 atcagcaggg ggaatccctg ccctggagcg ccctggctct ggactgcacc ccccttaggg 540  
38 ttgtcctgca gattctcttc cccatctttc tctgccacac acgcttccct aagccgcgc 600  
39 cgccgcaaac tcagtctcgg tccccgcagg tgatgtc atg ccc att gtt ttg gtg 655  
40 Met Pro Ile Val Leu Val  
41 1 5  
43 cgc cca acc aat cgg act cgc cgc ctg gat tct acc gga gcc ggc atg 703  
44 Arg Pro Thr Asn Arg Thr Arg Arg Leu Asp Ser Thr Gly Ala Gly Met  
45 10 15 20  
47 ggc cct tcc tcg cac cag cag cag gag tcc ccg ctc ccg acc ata acg 751  
48 Gly Pro Ser Ser His Gln Gln Gln Glu Ser Pro Leu Pro Thr Ile Thr  
49 25 30 35  
51 cat tgc gca ggg tgc acc acc gct tgg tct ccc tgc agc ttt aac agc 799  
52 His Cys Ala Gly Cys Thr Ala Trp Ser Pro Cys Ser Phe Asn Ser  
53 40 45 50  
55 cct gac atg gaa acc cca ttg cag ttc cag cgc ggc ttc ttc cca gag 847  
56 Pro Asp Met Glu Thr Pro Leu Gln Phe Gln Arg Gly Phe Phe Pro Glu  
57 55 60 65 70  
59 cag ccg ccg ccg ccg cgc tcc tca cac ctg cat tgc cag cag cag 895  
60 Gln Pro Pro Pro Pro Arg Ser Ser His Leu His Cys Gln Gln Gln  
61 75 80 85  
63 caa cag agc cag gac aag ccg tgc ccg ccc ttc gcg ccc ctc ccg cac 943

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64	Gln	Gln	Ser	Gln	Asp	Lys	Pro	Cys	Pro	Pro	Phe	Ala	Pro	Leu	Pro	His		
65				90			95					100						
67	cct	cac	cac	cac	ccg	cac	ctc	gcg	cac	cag	cag	ccg	gcc	agc	ggc	ggc	991	
68	Pro	His	His	His	Pro	His	Leu	Ala	His	Gln	Gln	Pro	Ala	Ser	Gly	Gly		
69				105				110				115						
71	agc	agc	cca	tgc	ctc	cg	tgc	aac	agc	tgc	gcc	tcc	tcc	ggt	gcc	ccg	1039	
72	Ser	Ser	Pro	Cys	Leu	Arg	Cys	Asn	Ser	Cys	Ala	Ser	Ser	Gly	Ala	Pro		
73				120			125				130							
75	gcg	g	gg	g	gg	g	g	at	a	c	t	g	t	c	t	c	1087	
76	Ala	Ala	Gly	Ala	Gly	Asp	Asn	Leu	Ser	Leu	Leu	Leu	Arg	Thr	Ser	Ser		
77	135				140				145				150					
79	ccc	ggc	ggc	gcc	ttc	cg	gg	acc	cgc	acc	tcc	tcg	ccg	ctg	tcg	ggc	tcg	1135
80	Pro	Gly	Gly	Ala	Phe	Arg	Thr	Arg	Thr	Ser	Ser	Pro	Leu	Ser	Gly	Ser		
81					155				160			165						
83	tcc	tgc	tgc	tgc	tgc	tgc	tcg	tcg	cgc	tcg	ccg	agc	cag	ctc	aat		1183	
84	Ser	Cys	Cys	Cys	Cys	Ser	Ser	Arg	Arg	Gly	Ser	Gln	Leu	Asn				
85					170			175				180						
87	gtg	agc	gag	ctg	acg	ccg	tcc	agc	cat	gcc	agt	g	ctc	ccg	cag	cag	1231	
88	Val	Ser	Glu	Leu	Thr	Pro	Ser	Ser	His	Ala	Ser	Ala	Leu	Arg	Gln	Gln		
89					185			190			195							
91	tac	g	cg	cag	tcc	g	cg	cag	tcg	g	cg	tcc	gcc	tcc	cag	tac	1279	
92	Tyr	Ala	Gln	Gln	Ser	Ala	Gln	Gln	Ser	Ala	Ser	Ala	Ser	Gln	Tyr	His		
93					200			205			210							
95	cag	tgc	cac	agc	ctg	cag	ccc	gcc	gcc	agc	ccc	acg	ggc	agc	ctc	ggc	1327	
96	Gln	Cys	His	Ser	Leu	Gln	Pro	Ala	Ala	Ser	Pro	Thr	Gly	Ser	Leu	Gly		
97	215				220			225				230						
99	agt	ctg	ggc	tcc	ggg	ccc	ccg	ctc	tcg	cac	cac	cac	cac	ccg	cac		1375	
100	Ser	Leu	Gly	Ser	Gly	Pro	Pro	Leu	Ser	His	His	His	His	His	Pro	His		
101					235			240			245							
103	ccg	g	cg	cac	cac	cac	cac	cac	cac	ccc	ccg	ccg	ccg	ccg	ccg	ccg	1423	
104	Pro	Ala	His	His	His	Gln	His	His	Gln	Pro	Gln	Ala	Arg	Arg	Glu	Ser	Asn	
105					250			255			260							
107	ccc	ttc	acc	gaa	ata	gcc	atg	agc	agc	tgc	agg	tac	aac	ggg	ggc	gtc	1471	
108	Pro	Phe	Thr	Glu	Ile	Ala	Met	Ser	Ser	Cys	Arg	Tyr	Asn	Gly	Gly	Val		
109					265			270			275							
111	atg	cg	ccg	ctc	agc	aa	ttg	agc	g	cg	tcc	cg	ccg	aa	ctg	cac	gag	1519
112	Met	Arg	Pro	Leu	Ser	Asn	Leu	Ser	Ala	Ser	Arg	Arg	Asn	Leu	His	Glu		
113					280			285			290							
115	atg	gac	tca	gag	g	cg	cag	ccc	ctg	cag	ccc	ccg	ccg	tct	gtc	gga	gga	1567
116	Met	Asp	Ser	Glu	Ala	Gln	Pro	Leu	Gln	Pro	Pro	Ala	Ser	Val	Gly	Gly		
117	295				300				305			310						
119	ggt	ggc	ggc	g	cg	tcc	ccg	tct	gca	g	cc	g	cc	g	cc	g	1615	
120	Gly	Gly	Gly	Ala	Ser	Ser	Pro	Ser	Ala									
121					315				320			325						
123	gtt	tgc	tcc	tca	g	cc	g	ag	atc	gt	gt	tct	aag	ccc	g	cac	aa	1663
124	Val	Ser	Ser	Ala	Pro	Glu	Ile	Val	Val	Ser	Lys	Pro	Glu	His	Asn			
125					330			335			340							
127	aac	tcc	aa	aa	ctg	g	cg	ctc	tat	g	ga	cc	gg	gg	gg	gg	act	1711
128	Asn	Ser	Asn	Asn	Leu	Ala	Leu	Tyr	Gly	Thr	Gly	Gly	Gly	Ser	Thr			

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129	345	350	355	
131	gga gga ggc ggc ggt ggc ggg agc ggg cac ggc agc agc agt ggc			1759
132	Gly Gly Gly Gly Gly Gly Ser Gly His Gly Ser Ser Ser Gly			
133	360	365	370	
135	acc aag tcc agc aaa aag aaa aac cag aac atc ggc tac aag ctg ggc			1807
136	Thr Lys Ser Ser Lys Lys Asn Gln Asn Ile Gly Tyr Lys Leu Gly			
137	375	380	385	390
139	cac cgg cgc gcc ctg ttc gaa aag cgc aag cgg ctc agc gac tac gcg			1855
140	His Arg Arg Ala Leu Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr Ala			
141	395	400	405	
143	ctc atc ttc ggc atg ttc ggc atc gtg gtc atg gtc atc gag acc gag			1903
144	Leu Ile Phe Gly Met Phe Gly Ile Val Val Met Val Ile Glu Thr Glu			
145	410	415	420	
147	ctg tcg tgg ggc gcc tac gac aag gcg tcg ctg tat tcc tta gct ctg			1951
148	Leu Ser Trp Gly Ala Tyr Asp Lys Ala Ser Leu Tyr Ser Leu Ala Leu			
149	425	430	435	
151	aaa tgc ctt atc agt ctc tcc acg atc atc ctg ctc ggt ctg atc atc			1999
152	Lys Cys Leu Ile Ser Leu Ser Thr Ile Ile Leu Leu Gly Leu Ile Ile			
153	440	445	450	
155	gtg tac cac gcc agg gaa ata cag ttg ttc atg gtg gac aat gga gca			2047
156	Val Tyr His Ala Arg Glu Ile Gln Leu Phe Met Val Asp Asn Gly Ala			
157	455	460	465	470
159	gat gac tgg aga ata gcc atg act tat gag cgt att ttc ttc atc tgc			2095
160	Asp Asp Trp Arg Ile Ala Met Thr Tyr Glu Arg Ile Phe Phe Ile Cys			
161	475	480	485	
163	ttg gaa ata ctg gtg tgt gct att cat ccc ata cct ggg aat tat aca			2143
164	Leu Glu Ile Leu Val Cys Ala Ile His Pro Ile Pro Gly Asn Tyr Thr			
165	490	495	500	
167	ttc aca tgg acg gcc cgg ctt gcc ttc tcc tat gcc cca tcc aca acc			2191
168	Phe Thr Trp Thr Ala Arg Leu Ala Phe Ser Tyr Ala Pro Ser Thr Thr			
169	505	510	515	
171	acc gct gat gtg gat att att tta tct ata cca atg ttc tta aga ctc			2239
172	Thr Ala Asp Val Asp Ile Ile Leu Ser Ile Pro Met Phe Leu Arg Leu			
173	520	525	530	
175	tat ctg att gcc aga gtc atg ctt tta cat agc aaa ctt ttc act gat			2287
176	Tyr Leu Ile Ala Arg Val Met Leu Leu His Ser Lys Leu Phe Thr Asp			
177	535	540	545	550
179	acc tcc tct aga agc att gga gca ctt aat aag ata aac ttc aat aca			2335
180	Thr Ser Ser Arg Ser Ile Gly Ala Leu Asn Lys Ile Asn Phe Asn Thr			
181	555	560	565	
183	cgt ttt gtt atg aag act tta atg act ata tgc cca gga act gta ctc			2383
184	Arg Phe Val Met Lys Thr Leu Met Thr Ile Cys Pro Gly Thr Val Leu			
185	570	575	580	
187	ttg gtt ttt agt atc tca tta tgg ata att gcc gca tgg act gtc cga			2431
188	Leu Val Phe Ser Ile Ser Leu Trp Ile Ile Ala Ala Trp Thr Val Arg			
189	585	590	595	
191	gct tgt gaa agg tac cat gat caa cag gat gtt act agc aac ttc ctt			2479
192	Ala Cys Glu Arg Tyr His Asp Gln Gln Asp Val Thr Ser Asn Phe Leu			
193	600	605	610	

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195	gga	gcf	atg	tgg	ttg	ata	tca	ata	act	ttt	ctc	tcc	att	ggt	tat	ggt	2527	
196	Gly	Ala	Met	Trp	Leu	Ile	Ser	Ile	Thr	Phe	Leu	Ser	Ile	Gly	Tyr	Gly		
197	615				620						625					630		
199	gac	atg	gta	cct	aac	aca	tac	tgt	gga	aaa	gga	gtc	tgc	tta	ctt	act	2575	
200	Asp	Met	Val	Pro	Asn	Thr	Tyr	Cys	Gly	Lys	Gly	Val	Cys	Leu	Leu	Thr		
201							635			640					645			
203	gga	att	atg	ggt	gct	ggt	tgc	aca	gcc	ctg	gtg	gta	gct	gta	gtg	gca	2623	
204	Gly	Ile	Met	Gly	Ala	Gly	Cys	Thr	Ala	Leu	Val	Val	Ala	Val	Val	Ala		
205							650		655		660							
207	agg	aag	cta	gaa	ctt	acc	aaa	gca	gaa	aaa	cac	gtg	cac	aat	ttc	atg	2671	
208	Arg	Lys	Leu	Glu	Leu	Thr	Lys	Ala	Glu	Lys	His	Val	His	Asn	Phe	Met		
209							665		670		675							
211	atg	gat	act	cag	ctg	act	aaa	aga	gta	aaa	aat	gca	gct	gcc	aat	gta	2719	
212	Met	Asp	Thr	Gln	Leu	Thr	Lys	Arg	Val	Lys	Asn	Ala	Ala	Ala	Asn	Val		
213							680		685		690							
215	ctc	agg	gaa	aca	tgg	cta	att	tac	aaa	aat	aca	aag	cta	gtg	aaa	aag	2767	
216	Leu	Arg	Glu	Thr	Trp	Leu	Ile	Tyr	Lys	Asn	Thr	Lys	Leu	Val	Lys	Lys		
217							695		700		705		710					
219	ata	gat	cat	gca	aaa	gta	aga	aaa	cat	caa	cga	aaa	ttc	ctg	caa	gct	2815	
220	Ile	Asp	His	Ala	Lys	Val	Arg	Lys	His	Gln	Arg	Lys	Phe	Leu	Gln	Ala		
221							715		720		725							
223	att	cat	caa	tta	aga	agt	gta	aaa	atg	gag	cag	agg	aaa	ctg	aat	gac	2863	
224	Ile	His	Gln	Leu	Arg	Ser	Val	Lys	Met	Glu	Gln	Arg	Lys	Leu	Asn	Asp		
225							730		735		740							
227	caa	gca	aac	act	ttg	gtg	gac	ttg	gca	aag	acc	cag	aac	atc	atg	tat	2911	
228	Gln	Ala	Asn	Thr	Leu	Val	Asp	Leu	Ala	Lys	Thr	Gln	Asn	Ile	Met	Tyr		
229							745		750		755							
231	gat	atg	att	tct	gac	tta	aac	gaa	agg	agt	gaa	gac	ttc	gag	aag	agg	2959	
232	Asp	Met	Ile	Ser	Asp	Leu	Asn	Glu	Arg	Ser	Glu	Asp	Phe	Glu	Lys	Arg		
233							760		765		770							
235	att	gtt	acc	ctg	gaa	aca	aaa	cta	gag	act	ttg	att	ggt	agc	atc	cac	3007	
236	Ile	Val	Thr	Leu	Glu	Thr	Lys	Leu	Glu	Thr	Leu	Ile	Gly	Ser	Ile	His		
237							775		780		785		790					
239	gcc	ctc	cct	ggg	ctc	ata	agc	cag	acc	atc	agg	cag	cag	cag	aga	gat	3055	
240	Ala	Leu	Pro	Gly	Leu	Ile	Ser	Gln	Thr	Ile	Arg	Gln	Gln	Arg	Asp			
241							795		800		805							
243	tcc	att	gag	gct	cag	atg	gag	agc	tac	gac	aag	cac	gtc	act	tac	aat	3103	
244	Phe	Ile	Glu	Ala	Gln	Met	Glu	Ser	Tyr	Asp	Lys	His	Val	Thr	Tyr	Asn		
245							810		815		820							
247	gct	gag	cg	tcc	cg	tcc	tcg	tcc	agg	agg	cg	cg	tcc	tct	tcc	aca	3151	
248	Ala	Glu	Arg	Ser	Arg	Ser	Ser	Arg	Arg	Arg	Arg	Arg	Ser	Ser	Ser	Thr		
249							825		830		835							
251	gca	cca	cca	act	tca	tca	gag	agt	agc	tagaagagaa	taagtttacc						3198	
252	Ala	Pro	Pro	Thr	Ser	Ser	Glu	Ser	Ser									
253							840		845									
255	acaaaataa	g	act	tttttgc	c	atcatat	ggt	caat	at	tta	gct	ttt	tatt	g	taa	agcccct	3258	
256	atgg	ttctaa	tc	agc	gtt	tt	ccgg	gg	ttc	at	gtc	aga	at	c	tga	acactaa	3318	
257	gtt	tttagg	cc	aaa	at	gag	tg	aa	act	ttt	ttt	c	at	g	caca	ggaa	atgcac	3378
258	ct	att	att	gc	tat	at	gat	tt	tt	c	c	t	a	ttt	ttt	at	tcatgcactt	3438

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259 caaacaaact ttactactac attatatgat atataataaa aaaagttaat ttctgcaaaa 3498  
260 aaaaaaaaaa aaaaaaaaaac ggacggg 3525  
262 <210> SEQ ID NO: 2  
263 <211> LENGTH: 847  
264 <212> TYPE: PRT  
265 <213> ORGANISM: Homo sapiens  
267 <400> SEQUENCE: 2  
268 Met Pro Ile Val Leu Val Arg Pro Thr Asn Arg Thr Arg Arg Leu Asp  
269 1 5 10 15  
270 Ser Thr Gly Ala Gly Met Gly Pro Ser Ser His Gln Gln Gln Glu Ser  
271 20 25 30  
272 Pro Leu Pro Thr Ile Thr His Cys Ala Gly Cys Thr Thr Ala Trp Ser  
273 35 40 45  
274 Pro Cys Ser Phe Asn Ser Pro Asp Met Glu Thr Pro Leu Gln Phe Gln  
275 50 55 60  
276 Arg Gly Phe Phe Pro Glu Gln Pro Pro Pro Pro Arg Ser Ser His  
277 65 70 75 80  
278 Leu His Cys Gln Gln Gln Gln Ser Gln Asp Lys Pro Cys Pro Pro  
279 85 90 95  
280 Phe Ala Pro Leu Pro His Pro His His Pro His Leu Ala His Gln  
281 100 105 110  
282 Gln Pro Ala Ser Gly Gly Ser Ser Pro Cys Leu Arg Cys Asn Ser Cys  
283 115 120 125  
284 Ala Ser Ser Gly Ala Pro Ala Ala Gly Ala Gly Asp Asn Leu Ser Leu  
285 130 135 140  
286 Leu Leu Arg Thr Ser Ser Pro Gly Gly Ala Phe Arg Thr Arg Thr Ser  
287 145 150 155 160  
288 Ser Pro Leu Ser Gly Ser Ser Cys Cys Cys Cys Cys Ser Ser Arg  
289 165 170 175  
290 Arg Gly Ser Gln Leu Asn Val Ser Glu Leu Thr Pro Ser Ser His Ala  
291 180 185 190  
292 Ser Ala Leu Arg Gln Gln Tyr Ala Gln Gln Ser Ala Gln Gln Ser Ala  
293 195 200 205  
294 Ser Ala Ser Gln Tyr His Gln Cys His Ser Leu Gln Pro Ala Ala Ser  
295 210 215 220  
296 Pro Thr Gly Ser Leu Gly Ser Leu Gly Ser Gly Pro Pro Leu Ser His  
297 225 230 235 240  
298 His His His His Pro Ala His His Gln His His Gln Pro Gln  
299 245 250 255  
300 Ala Arg Arg Glu Ser Asn Pro Phe Thr Glu Ile Ala Met Ser Ser Cys  
301 260 265 270  
302 Arg Tyr Asn Gly Gly Val Met Arg Pro Leu Ser Asn Leu Ser Ala Ser  
303 275 280 285  
304 Arg Arg Asn Leu His Glu Met Asp Ser Glu Ala Gln Pro Leu Gln Pro  
305 290 295 300  
306 Pro Ala Ser Val Gly Gly Gly Gly Ala Ser Ser Pro Ser Ala Ala  
307 305 310 315 320  
308 Ala Ala Ala Ala Ala Val Ser Ser Ser Ala Pro Glu Ile Val Val  
309 325 330 335

VERIFICATION SUMMARY  
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date